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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/032,717	10/23/2001	Andre R. Abad	35718/237005 (5718-118)	5409

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EXAMINER	
KUBELIK, ANNE R	
ART UNIT	**PAPER NUMBER**
1638	

DATE MAILED: 05/06/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/032,717	ABAD ET AL.	
	Examiner	Art Unit	
	Anne R. Kubelik	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *21 January 2005*.

2a)☒ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-3,9-12,17-19,38-40,43-46,49-52 and 55-65* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-3,9-12,17-19,38,43,46,49,52 and 55-65* is/are rejected.

7)☒ Claim(s) *39,40,44,45,50 and 51* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *search notes*.

DETAILED ACTION

1. Claims 1-3, 9-12, 17-19, 38-40, 43-46, 49-52 and 55-65 are pending.

2. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

3. The rejection of claims 1-3, 9-12, 17-19, 46, 52, 57 and 60-62 under 35 U.S.C. 103(a) as being unpatentable over Michaels et al (1996, US Patent 5,554,534) is withdrawn in light of the analysis and Declarations of Drs. McNeill and C Simmons.

Claim Rejections - 35 USC § 112

4. Claims 1-3, 9-12, 17-19, 38, 43, 46, 49, 52 and 55-65 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for nucleic acids encoding SEQ ID NO:2 and 10, expression cassettes comprising the nucleic acids, plants and seeds comprising a construct comprising the nucleic acid, and a method of using it to impact a plant pest, does not reasonably provide enablement for any nucleic acid that has 90% identity to SEQ ID NO:1, expression cassettes comprising the nucleic acid, plants and seeds comprising a construct comprising the nucleic acid and a method of using it to impact a plant pest. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims. The rejection is modified from the rejection set forth in the Office action mailed 21 October 2004, as applied to claims 1-3, 9-12, 17-19, 38, 43, 46, 49, 52 and 55-64. Applicant's arguments and the Declaration of Dr. Abad, both filed 21 January 2005, have been fully considered but they are not persuasive.

Applicant urges that limiting the claims to only the exact exemplary sequences is unreasonable because it is relatively simple to modify a nucleic acid and amino acid sequence at a few positions to generate a protein that retains the full activity of the original, and would not give Applicant any meaningful protection (response pg 7-8).

This is not found persuasive. The claims are not drawn to modification of only a few positions, but to modification of up to 362 nucleotides or amino acids. If, as Applicant contends, it is "relatively simple" to modify 362 nucleotides, then it would also be "relatively simple" to modify 363 nucleotides, thus avoiding the scope of the claim. Thus, applicant's argument about teaching the public to make and use the invention without obtaining any protection it contradictory to Applicant's argument that nucleic acids with 90% identity to SEQ ID NO:1 are enabled.

Applicant urges that claims to nucleic acids with 93%, 94% and 95% identity would meet the patentability requirements even if specified percentages well below 90%; these claims have been ignored, however (response pg 8).

This is not found persuasive. Nucleic acids that have 93% identity to SEQ ID NO:1 would have up to 253 nucleotide substitutions and up to 253 amino acid substitutions, nucleic acids that have 94% identity to SEQ ID NO:1 would have up to 217 nucleotide substitutions and up to 217 amino acid substitutions, and nucleic acids that have 95% identity to SEQ ID NO:1 would have up to 181 nucleotide substitutions and up to 181 amino acid substitutions. The specification does not teach how to make nucleic acids encoding pesticidal proteins with 181, 217 or 253 substitutions.

Applicant urges that guidance is provided as to what sequence alterations may be made and still provide a pesticidal polypeptide; endotoxin genes are well known in the art, an

exemplary sequence was provided, the claimed sequences differ from the exemplary by structural parameters, and guidance for determining percent identity is given on pg 33-38 (response pg 9).

This is not found persuasive because the specification does not teach how to make nucleic acids encoding Coleopteran pesticidal proteins with 181, 217, 253 or 362 substitutions. Guidance for determining percent identity does not teach the necessary and sufficient structural features of the claimed nucleic acids

Applicant urges that support is provided for the functional limitation, guidance is provided in that the alterations should be conservation substitutions and have particular activity. Applicant urges that while not every nucleic acid that meets the identity limitations will have the function, one of skill in the art could make and use the nucleic acids because methods for assaying pesticidal activity are routine and demonstrated in the specification (response pg 10).

This is not found persuasive because the specification only suggests inserting trypsin and chymotrypsin digestion sites and suggests making variants by deleting, substituting or inserting one or more amino acids, but do not provide guidance as to which amino acids to delete, substitute or insert, other than the insertion of a few amino acids. The specification does not teach how to make nucleic acids encoding Coleopteran pesticidal proteins with 181, 217, 253 or 362 substitutions. Variants within the full scope of the claims are not taught.

Applicant urges that Bt toxins are very well-characterized, and that the specification uses Li et al for guidance in making mutations in the Cry8-like proteins, as in Example 6; thus, adequate guidance is provided (response pg 10-11).

This is not found persuasive. Li et al only provided guidance for making truncations and insertion of chymotrypsin cleavage sites; Li et al do not provide guidance for making 181, 217,

253 or 362 amino acid substitutions in a 1206 amino acid protein. Furthermore, the protein taught by Li et al is a cry3Aa protein, not a Cry8 protein.

Applicant urges that Li et al teaches the tertiary structure of an exemplary Cry endotoxin, and the instant inventors were able to use the extensive knowledge in the art to modify the exemplary sequences to make variant endotoxins (response pg 11-12).

This is not found persuasive because the instant inventors did not use Li et al to make 181, 217, 253 or 362 amino acid substitutions in a 1206 amino acid protein to create a Coleopteran pesticidal protein.

Applicant urges that those of skill in the art are aware of conserved regions of the Cry endotoxins and can use the Pfam database to determine protein function and conserved regions and regions that are more likely to tolerate mutations (response pg 12).

This is not found persuasive. This database search provides no guidance as to the relevance to the sequence segments that are responsible for the pesticidal specificity of the proteins (see Li et al, pg 815, left column). Additionally, the Pfam database results sent by Applicant give no indication what, if any, of the information sent was available in the database at the time of filing. Lastly, the specification does not teach using this database. See *Genentech, Inc. v. Novo Nordisk, A/S*, 42 USPQ2d 1001, 1005 (Fed. Cir. 1997), which teaches that disclosure of a "mere germ of an idea does not constitute [an] enabling disclosure", and that "the specification, not the knowledge of one skilled in the art" must supply the enabling aspects of the invention.

Applicant urges that the specification teaches several nucleic acids with low percent identity to SEQ ID NO:1 but that encode pesticidal proteins. In Examples 4 and 6, truncated proteins encoded by SEQ ID NO:15 and 19 are described; they have 55% and 51% identity to

SEQ ID NO:1, respectively, and is structurally very different from SEQ ID NO:1 (response pg 12-13).

This is not found persuasive. The specification teaches a fragment, in the form of SEQ ID NO:15, but does not teach an additional sequence. While the query match similarity between the truncated proteins encoded by SEQ ID NO:15 and 19 may be 55% and 51% to SEQ ID NO:1, respectively, the query match value is affected by differences in length of the sequences. One of skill in the art would not consider a truncated protein as having 55% identity over its entire length, but would only look at it as a truncated protein. The local match similarity between SEQ ID NO:15 and the first half of SEQ ID NO:1 is 100%; thus SEQ ID NO:15 does not teach which 181, 217, 253 or 362 amino acids to substitute in SEQ ID NO:2.

Applicant urges that Example 6 also teaches the truncated protein encoded by SEQ ID NO:11 which also has a four amino insertion in it; SEQ ID NO:11 has 56% identity to SEQ ID NO:1. Applicant also urges that the specification teaches a maize-optimized sequence that encodes SEQ ID NO:16 but has less than 69% identity to SEQ ID NO:15 (response pg 13-14).

This is not found persuasive. SEQ ID NO:11 only provides guidance for a single insertion of 4 amino acids in the 669 amino acid long SEQ ID NO:16 and does not provide guidance for nucleic acids encoding proteins with 70% identity to SEQ ID NO:2, which nucleic acids with 90% identity to SEQ ID NO:1 encompass). No amino acid substitutions were made in the protein sequence encoded by SEQ ID NO:15. Nucleic acids encoding SEQ ID NO:16 are enabled, and this is true regardless of their identity to SEQ ID NO:15. What is not enabled is nucleic acids encoding proteins with 181, 217, 253 or 362 amino acid substitutions relative to SEQ ID NO:2.

Applicant urges that the specification does not teach only a fragment and a single 4 amino acid substitution and has not provided guidance for making up to 362 amino acid substitutions, as they have provided percent identity variants that include both fragments and amino acid changes and have taught representative species of the genus; furthermore there is extensive knowledge in the art about the structure and function of endotoxins, thus equipping one of skill in the art to identify which portions of the disclosed sequence are more conserved and which would tolerate mutations (response pg 14).

This is not found persuasive because the percent identity variants taught by the specification do not represent the full scope of the claims. Making a fragment and a single 4 amino acid substitution are not the same thing as making 362 amino acid substitutions. It is "the specification, not the knowledge of one skilled in the art" that must supply the enabling aspects of the invention (*Genentech, Inc. v. Novo Nordisk, A/S*, 42 USPQ2d 1001, 1005 (Fed. Cir. 1997).

Applicant urges that the amount of experimentation required is not undue as provided by the working examples and reports in the art of similar experimentation, citing Wu et al (response pg).

This is not found persuasive. Wu et al only modified 4 amino acids, not 181, 217, 253 or 362 amino acids. None of the working examples in the specification modified 181, 217, 253 or 362 amino acids.

Applicant urges that the quality of experimentation required to make the claimed nucleic acids amounts to two steps, making the nucleic acid and assaying the encoded protein for activity; thus, experimentation is not undue, and provide the Declaration of Dr. Abad (response pg 15).

This is not found persuasive. Assays for the protein are more detailed than assays for enzymatic activity; the latter can often be easily assayed spectrophotographically. The assays

detailed in Examples 4, 6 and 7 require expressing the proteins in E. coli, purifying the protein from large scale cultures of the bacteria via affinity chromatography followed by extensive dialysis, and incorporating the protein into the diets of rootworms in replicates of 4, with mortality measured on the 4th to 7th day (Examples 4, 6 and 7); thus, each assay requires up to two weeks and large quantities of materials. As guidance is not provided for making up to 362 amino acid substitutions in a 1206 amino acid protein, undue trial and error experimentation would be required to make and to assay vast numbers of nucleic acids in order to find any that fell within the scope of the claims.

Dr. Abad states that he would be able to make and use the claimed nucleic acids by making nucleic acids with 90% identity to SEQ ID NO:1 and assaying the activity of the encoded protein and would consider this experimentation routine. It is also his understanding that proteins can be produced that share a relatively low degree of sequence identity, maybe even as low as 70% identity (Declaration ¶2-3).

This is not found persuasive. The Declaration only provides opinions, and ones the Declarant is not even sure of.

Applicant urges that the amount of experimentation required to practice the identity claims is not undue, because plant transformation and DNA constructs are routine (response pg 15-16).

This is not found persuasive. Plant transformation and construct of DNA constructs, per se, are enabled. What is not enabled is making the nucleic acids required to make the claimed plants and constructs, that is nucleic acids encoding proteins with 181, 217, 253 or 362 amino acid substitutions in a 1206 amino acid protein, given the lack of guidance provided in the specification.

Applicant urges that it is customary in the art to make and assay sequences, for example by shuffling, as described in US 5,837,458. Applicant also cites Minshull et al and Christians et al, and urges that these methods are designed to generate and test a very large number of variant sequences (response pg 16).

This is not found persuasive. With respect to using DNA shuffling, the specification, on pg 29, suggests using GenBank U04365, which is identical to SEQ ID NO:3 of Michaels et al (1996, US Patent 5,554,534), as the other nucleic acid in shuffling; however, this sequence encodes a protein with 79.8% identity to the instant SEQ ID NO:2. Thus, it is unlikely that it could be used to generate a nucleic acid that encodes a protein with 70% identity to SEQ ID NO:2. Christians et al did not produce proteins with only 70% identity to the starting protein (see paragraph spanning pg 260-261). Minshull et al teaches that a population should be used as the starting material (pg 284, right column, paragraph 4); the specification does not teach such a population. Minshull et al also teaches that the activities of chimeric enzymes are not predictable simply by comparing those of the parent enzymes (paragraph spanning pg 288-289); thus, , even if the population of starting materials has been provided, making nucleic acids that encode proteins pesticidal to coleopterans and have substitutions within the full scope of the claims is not predictable. could not be considered because they were not sent.

Applicant urges that inoperative embodiments do not render the claims invalid and undue experimentation would not required to test a protein for pesticidal activity; Lazar et al and Hill et al illustrate that one would be able to determine whether a particular sequence change affected the function of a protein (response pg 17-18).

This is not found persuasive. As discussed above, undue trial and error experimentation would be required to make and to assay vast numbers of nucleic acids in order to find any that

fell within the scope of the claims. Neither Lazar et al nor Hill et al needed to engage in undue trial and error experimentation; thus, their use in response to an argument about trial and error experimentation is off point.

Applicant urges that in Wands the experimentation required was not found undue (response pg 18-19).

This is not found persuasive because making all possible single amino acid substitutions, in an 3621 nucleotide long nucleic acid like that of SEQ ID NO:1 would require making and analyzing 19^{3621} nucleic acids; these nucleic acids would have about 99.99% identity to SEQ ID NO:1. Making the nucleic acids this way would be required because of the lack of guidance provided in the specification. Thus, in the instant case, the amount of experimentation required would be undue.

It is noted that the specification teaches does not teach nucleic acids comprising 50 nucleotide segments of SEQ ID NO:1 within the full scope of the claims. The only such molecules taught in the specification are SEQ ID NO:15 and 19.

5. Claims 1-3, 9-12, 17-19, 38, 43, 46, 49, 52 and 55-65 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The rejection is repeated for the reasons of record as set forth in the Office action mailed 21 October 2004, as applied to claims 1-3, 9-12, 17-19, 38, 42-43,46, 48-49, 52 and 54-64. Applicant's arguments filed 21 January 2005 have been fully considered but they are not persuasive.

Applicant urges that that because the claimed nucleic acids are defined in relation to SEQ ID NO:1, they have provided a structural definition of the sequences, and because they have

provide assays for one of skill in that to assess whether those sequences meet the functional limitation of the claims, they have met the requirements of *Eli Lilly* and *Amgen*, also citing *Amgen vs Hoechst*, *Moba* and *Enzo* (response pg 20-21).

This is not found persuasive. *Eli Lilly* at pg 1406 states "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus." A single nucleic acid of SEQ ID NO:1 does not constitute a significant portion of the genus of nucleic acids with 90% identity to SEQ ID NO:1. The specification does not describe the structural features that distinguish nucleic acids with 90% identity to SEQ ID NO:1 that encode pesticidal proteins from nucleic acids with 90% identity to SEQ ID NO:1 that do not encode pesticidal proteins. *Enzo* states that a deposited sequence meets the written description requirement; no nucleic acid with 90% identity to a known sequence and that encodes a protein with 70% identity to the original protein has been deposited by Applicant, nor has any other nucleic acid within the scope of the claims. In the instant case the knowledge of the art the disclosed function is not sufficiently correlated to a particular, known structure; which 362 amino acids can be substituted in SEQ ID NO:2 is unknown.

Applicant urges that Bt toxins are very well-characterized, and that the specification uses Li et al for guidance in making mutations in the Cry8-like proteins, as in Example 6; thus, adequate guidance is provided (response pg 21-22).

This is not found persuasive. Li et al only provided guidance for making truncations and insertion of chymotrypsin cleavage sites; Li et al do not provide guidance for making 362 amino

acid substitutions in a 1206 amino acid protein. Additionally, Applicant's arguments are drawn to an enablement rejection, not a written description rejection.

Applicant urges that one of skill in the art could use the Pfam database to make the claimed nucleic acids, thus they have envisioned the detailed construction of the gene (response pg 22).

This is not found persuasive. The specification does not describe the necessary and sufficient structural features for nucleic acids with 90% identity to SEQ ID NO:1 and that encode a protein that is pesticidal to Coleopterans within the full cope of the claims, and from what was sent in Appendix B, neither does the Pfam database. Additionally, the Pfam database results sent by Applicant give no indication what, if any, of the information sent was available in the database at the time of filing.

Applicant urges that the specification describes several nucleic acids with low percent identity to SEQ ID NO:1 but that encode pesticidal proteins. In Examples 4 and 6, truncated proteins encoded by SEQ ID NO:15 and 19 are described; they have 55% and 51% identity to SEQ ID NO:1, respectively. Example 6 also teaches the truncated protein encoded by SEQ ID NO:11 which also has a four amino insertion in it; SEQ ID NO:11 has 56% identity to SEQ ID NO:1. Applicant also urges that the specification teaches a maize-optimized sequence that encodes SEQ ID NO:16 but has less than 69% identity to SEQ ID NO:15 (response pg 23).

This is not found persuasive. The Office is not dismissing the teachings in the specification with regard to the fragments and variant taught in the specification; the Office is saying that they are not sufficient to describe nucleic acid within the full scope of the claims. While the query match similarity may be 55%, the query match value is affected by differences in length of the sequences. No amino acid substitutions were made in the protein sequence

encoded by SEQ ID NO:15, thus, this nucleic acid does not describe nucleic acids encoding proteins with 181, 217, 253 or 362 amino acid substitutions relative to SEQ ID NO:2.

Applicant urges that they disagree with the assessment of the significance exemplary proteins, so that one of skill in the art would recognize what portions of the protein are most significant (response pg 23-24).

This is not found persuasive. The claims encmompass nucleic acids encoding proteins with 181, 217, 253 or 362 amino acid substitutions relative to SEQ ID NO:2. The specification does not describe such nucleic acid within the full scope of the claims. Where does the specification describe such a nucleic acid?

Claim Rejections - 35 USC § 102

6. Claim 65 is rejected under 35 U.S.C. 102(b) as being anticipated by Michaels et al (US Patent 5,556534).

Michaels et al teach a nucleic acid that comprises 50 nucleotides of SEQ ID NO:1 and encodes a protein that is pesticidal for Coleopterans (see search results).

7. Claims 39-40, 44-45 and 50-51 are objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

Conclusion

8. Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

9. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Anne R. Kubelik, whose telephone number is (571) 272-0801. The examiner can normally be reached Monday through Friday, 8:30 am - 5:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson, can be reached at (571) 272-0804. The central fax number for official correspondence is (571) 273-8300.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

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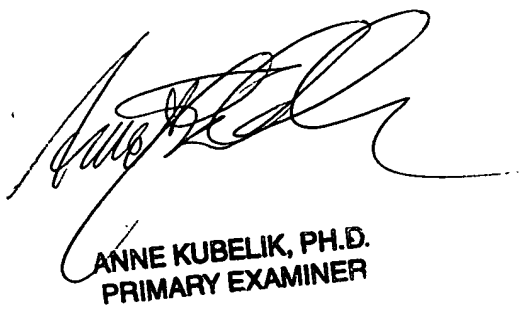
Anne R. Kubelik, Ph.D.
April 15, 2005



OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
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Searched: 441362 seqs, 153338381 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2565.2	70.8	3507	1	US-08-315-468-3	Sequence 3, Appli
2	1812.2	50.0	3471	1	US-07-876-280-29	Sequence 29, Appl
3	1812.2	50.0	3471	1	US-07-812-180A-1	Sequence 1, Appli
4	1812.2	50.0	3471	1	US-08-315-468-1	Sequence 1, Appli
5	1812.2	50.0	3471	4	US-07-941-650A-1	Sequence 1, Appli
6	1180	32.6	3797	1	US-07-915-203-1	Sequence 1, Appli
7	1180	32.6	3797	1	US-08-272-887-1	Sequence 1, Appli
8	1180	32.6	3797	1	US-08-789-449-1	Sequence 1, Appli
9	883.4	24.4	4344	2	US-08-532-547-4	Sequence 4, Appli
10	883.4	24.4	4344	2	US-08-379-656B-4	Sequence 4, Appli
11	883.4	24.4	4344	3	US-08-455-838-4	Sequence 4, Appli
12	883.4	24.4	4344	3	US-09-019-809-4	Sequence 4, Appli
13	883.4	24.4	4344	4	US-09-471-177-4	Sequence 4, Appli
14	882.8	24.4	3471	4	US-09-002-285-73	Sequence 73, Appl
15	848.6	23.4	3759	1	US-08-542-921-1	Sequence 1, Appli
16	848.6	23.4	3759	2	US-08-880-685-1	Sequence 1, Appli
17	848.6	23.4	3759	2	US-08-880-684-1	Sequence 1, Appli
18	822.2	22.7	3453	4	US-09-002-285-75	Sequence 75, Appl
19	734.2	20.3	3411	4	US-09-002-285-77	Sequence 77, Appl
20	733.6	20.3	3414	1	US-07-973-320-3	Sequence 3, Appli
21	731.4	20.2	3414	1	US-07-973-320-1	Sequence 1, Appli
22	678	18.7	3934	1	US-08-100-709-3	Sequence 3, Appli
23	678	18.7	3934	1	US-08-176-865-3	Sequence 3, Appli
24	678	18.7	3934	1	US-08-474-038-3	Sequence 3, Appli
25	678	18.7	3934	2	US-08-779-046-3	Sequence 3, Appli
26	678	18.7	3934	2	US-08-881-340-3	Sequence 3, Appli
27	673.6	18.6	4074	1	US-08-377-690-1	Sequence 1, Appli
28	659.2	18.2	3684	1	US-08-448-170-7	Sequence 7, Appli
29	659.2	18.2	3684	3	US-08-961-803-5	Sequence 5, Appli
30	618.6	17.1	3567	6	5188960-5	Patent No. 5188960
31	615.4	17.0	3567	2	US-08-980-071-5	Sequence 5, Appli
32	615.4	17.0	3567	2	US-08-980-071-58	Sequence 58, Appl
33	615.4	17.0	3567	2	US-08-757-536-5	Sequence 5, Appli
34	615.4	17.0	3567	3	US-09-314-093-5	Sequence 5, Appli
35	615.4	17.0	3567	3	US-09-314-093-58	Sequence 58, Appl
36	615.4	17.0	3567	3	US-09-250-848-5	Sequence 5, Appli
37	615.4	17.0	3567	4	US-09-251-885-5	Sequence 5, Appli
38	615.4	17.0	3567	4	US-09-337-635-5	Sequence 5, Appli
39	615.4	17.0	3567	4	US-09-337-635-58	Sequence 58, Appl
40	615.4	17.0	3567	4	US-09-337-280-5	Sequence 5, Appli
41	615.4	17.0	3567	4	US-09-337-280-58	Sequence 58, Appl
42	613.8	17.0	3567	1	US-08-602-737-1	Sequence 1, Appli
43	613.8	17.0	3567	2	US-08-980-071-1	Sequence 1, Appli
44	613.8	17.0	3567	2	US-08-980-071-9	Sequence 9, Appli
45	613.8	17.0	3567	2	US-08-980-071-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-315-468-3
; Sequence 3, Application US/08315468
; Patent No. 5554534
; GENERAL INFORMATION:
; APPLICANT: Michaels, Tracy Ellis
; APPLICANT: Foncerrada, Luis
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Process for Controlling Scarab Pests
; TITLE OF INVENTION: with Bacillus thuringiensis Isolates
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315,468
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,941
; FILING DATE: 01-FEB-1993
; APPLICATION NUMBER: 07/828,430
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/808,316
; FILING DATE: 16-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA73.C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3507 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: 50C
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGEM-11(tm) library of L. Foncerrada
; CLONE: 50C(b)
US-08-315-468-3

Query Match 70.8%; Score 2565.2; DB 1; Length 3507;
Best Local Similarity 85.1%; Pred. No. 0;
Matches 2906; Conservative 0; Mismatches 493; Indels 15; Gaps 3;

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Qy       1 ATGAGTCCAAATAATCAAAATGAATATGAAATTATAGATGCGACACCTTCTACTTCTGTA 60
Db       1 ATGAGTCCAAATAATCAAAATGAATATGAAATTATAGATGCGACACCTTCTACATCTGTA 60

Qy      61 TCCAATGATTCTAACAGATACCCTTTTGCGAATGAGCCAACAAATGCGCTACAAAATATG 120
Db      61 TCCAATGATTCTAACAGATACCCTTTTGCGAATGAGCCAACAAATGCGCTACAAAATATG 120

Qy     121 GATTATAAAGATTATTTAAAAATGTCTGCGGGAAATGCTAGTGAATACCCTGGTTCACCT 180
Db     121 GATTATAAAGATTATTTAAAAATGTCTGCGGGAAATGTTAGTGAATACCCTGGTTCACCT 180

Qy     181 GAAGTACTTGTTAGCGGACAAGATGCAGCTAAGGCCGCAATTGATATAGTAGGTAAATTA 240
Db     181 GAGGTATTTCTAAGCGAGCAAGATGCAGTTAAGGCCGCAATTGATATAGTAGGTAAATTA 240

Qy     241 CTATCAGGTTTAGGGGTCCCATTTGTTGGGCCGATAGTGAGTCTTTATACTCAACTTATT 300
Db     241 CTAACAGGTTTAGGGGTTCCATTTGTTGGGCCGATAGTGAGTCTTTATACTCAACTTATT 300

Qy     301 GATATTCTGTGGCCTTCAGGGAAAAGAGTCAATGGGAAATTTTTATGGAACAAGTAGAA 360
Db     301 GATATTCTGTGGCCTTCAAAACAAAAGAGTCAATGGGAAATTTTTATGGAACAAGTAGAA 360

Qy     361 GAACTCATTAATCAAAAAATAGCAGAATATGCAAGGAATAAAGCGCTTTCGGAATTAGAA 420
Db     361 GAACTCATTAATCAAAAAATAGCAGAATATGCAAGGAATAAAGCGCTTTCGGAATTGGAA 420

Qy     421 GGATTAGGTAATAATTACCAATTATATCTAACTGCGCTTGAAGAATGGGAAGAAAATCCA 480
Db     421 GGGCTAGGGAATAATTACCAATTATATCTAACTGCGCTTGAAGAGTGGAAAGAAAATCCA 480

Qy     481 AATGGTTCAAGAGCCTTACGAGATGTGCGAAATCGATTTGAAATCCTGGATAGTTTATTT 540
Db     481 AATGGTTCAAGAGCCTTACGAGATGTTCGAAATCGATTTGAAATCCTGGATAGTTTATTT 540

Qy     541 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATTCCTTACTGTATAT 600
Db     541 ACGCAATATATGCCATCTTTTCGAGTGACAAATTTTGAAGTACCATTCCTTACAGTATAT 600

Qy     601 GCAATGGCAGCCAACCTTCATTTACTGTTATTAAAGGACGCGTCAATTTTTGGAGAAGAA 660
Db     601 ACAATGGCAGCAAACCTACATTTACTTTTATTAAGGGACGCATCAATTTTTGGAGAAGAA 660

Qy     661 TGGGGATGGTCAACAACTACTATTAATAACTATTATGATCGTCAAATGAAACTTACTGCA 720
Db     661 TGGGGATTGTCTACAAGCACTATTAATAACTACTATAATCGTCAAATGAAACTTACTGCA 720

Qy     721 GAATATTCTGATCACTGTGTAAAGTGGTATGAAACTGGTTTAGCAAAATTAAAAGGCACG 780
Db     721 GAATATTCTGACCACTGTGTAAAGTGGTATGAAACTGGTTTAGCAAAATTAAAAGGCTCG 780

Qy     781 AGCGCTAAACAATGGGTTGACTATAACCAATTCCGTAGAGAAATGACACTGGCGGTTTTA 840
Db     781 AGCGCTAAACAATGGATTGACTATAACCAATTCCGTAGAGAAATGACATTGACGGTGTTA 840

Qy     841 GATGTTGTTGCATTATTCCCAAATTATGACACACGCACGTACCCAATGGAAACGAAAGCA 900
Db     841 GACGTTGTTGCATTATTTTCAAACTATGATACGCGTACGTATCCACTGGCAACAACAGCT 900

Qy     901 CAACTAACAAGGGAAGTATATACAGATCCACTGGGCGCGGTAAACGTGTCTTCAATTGGT 960
Db     901 CAGCTTACAAGGGAAGTATATACAGATCCACTTGGCGCGGTAGATGTGCCTAATATTGGC 960

Qy     961 TCCTGGTATGACAAAGCACCTTCTTTCGGAGTGATAGAATCATCCGTTATTCGACCACCC 1020
Db     961 TCCTGGTATGACAAAGCACCTTCTTTCTCAGAAATAGAAAAAGCGGCTATTCGTCCACCT 1020

Qy    1021 CATGTATTTGATTATATAACGGGACTCACAGTGTATACACAATCAAGAAGCATTTCTTCC 1080
Db    1021 CATGTGTTTGATTATATAACGGGACTCACAGTTTATACAAAAAAACGTAGCTTCACTTCT 1080

Qy    1081 GCTCGCTATATAAGACATTGGGCTGGTCATCAAATAAGCTACCATCGTGTCAGTAGGGGT 1140
Db    1081 GATCGTTATATGAGATATTGGGCTGGTCATCAAATAAGCTATAAGCATATCGGTACGAGT 1140

Qy    1141 AGTAATCTTCAACAAATGTATGGAACTAATCAAAATCTACACAGCACTAGTACCTTTGAT 1200
Db    1141 AGTACCTTTACACAGATGTATGGAACCAATCAAAATTTACAAAGTACTAGCAATTTTGAT 1200

Qy    1201 TTTACGAATTATGATATTTACAAGACTCTATCAAAGGATGCAGTACTCCTTGATATTGTT 1260
Db    1201 TTTACGAATTACGATATTTACAAGACTTTATCAAATGGTGCAGTACTCCTTGATATAGTT 1260

Qy    1261 TACCCTGGTTATACGTATATATTTTTTGGAATGCCAGAAGTCGAGTTTTTCATGGTAAAC 1320
Db    1261 TACCCTGGTTATACGTATACATTTTTTGGAATGCCAGAAACCGAGTTTTTTATGGTAAAT 1320

Qy    1321 CAATTGAATAATACCAGAAAGACGTTAAAGTATAATCCAGTTTCCAAAGATATTATAGCG 1380
Db    1321 CAATTGAATAATACCAGAAAGACGTTAACGTATAAACCAGCTTCCAAAGATATTATAGAT 1380

Qy    1381 AGTACAAGAGATTCGGAATTAGAATTACCTCCAGAAACTTCAGATCAACCAAATTATGAG 1440
Db    1381 CGGACAAGAGATTCGGAATTAGAATTGCCTCCAGAAACTTCAGGTCAACCAAATTACGAG 1440

Qy    1441 TCATATAGCCATAGATTATGTCATATCACAAGTATTCCCGCGACGGGTAACACTACCGGA 1500
Db    1441 TCATATAGCCATAGATTAGGTCATATTACATTTATTTACTCCA---GTTCAACTAGCACG 1497

Qy    1501 TTAGTACCTGTATTTTCTTGGACACATCGAAGTGCAGATTTAAACAATACAATATATTCA 1560
Db    1498 TATGTACCTGTATTTTCTTGGACACATCGGAGTGCAGATCTAACAAATACAGTTAAAAGT 1557

Qy    1561 GATAAAATCACTCAAATTCCGGCCGTTAAATGTTGGGATAATTTACCGTTTGTTCCAGTG 1620
Db    1558 GGCGAAATCACCCAAATACCAGGGGGCAAGTCTAGCACCATAGGCAGAAATACTTATATA 1617

Qy    1621 GTAAAAGGACCAGGACATACAGGAGGGGATTTATTACAGTATAATAGAAGTACTGGTTCT 1680
Db    1618 ATAAAAGGGCGTGGTTATACAGGGGGAGACTTAGTGGCTTTAACGGACCGCATCGGAAGT 1677

Qy    1681 GTAGGAACCTTATTTCTAGCTCGATATGGCCTAGCATTAGAAAAAGCAGGGAAATATCGT 1740
Db    1678 TGTGAGTTTCAGATGATCTTTCCAGAGTCTCAACGATTCCGTATTCGGATTCGTTACGCT 1737

Qy    1741 GTAAGACTGAGATATGCTACTGATGCAGATATTGTATTGCATGTAAACGATGCTCAGATT 1800
Db    1738 TCTAATGAAACTAGTTATATTAGTTTATACGGACTAAACCAAAGCGGAACTTTAAAATTC 1797

Qy    1801 CAGATGCCAAAAACAATGAACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCA 1860
Db    1798 AACCAGACATATTCTAATAAAAATGAAAATGATTTAACATATAATGATTTCAAATATATA 1857

Qy    1861 GATGCTATCACAACATTAAATTTAGCAACAGATAGTTCGCTAGCATTGAAACATAATTTA 1920
Db    1858 GAATATC---CAAGAGTCATTTCAGTAAATGCTTCTTCAAACATACAGAGGTTATCTATA 1914

Qy    1921 GGTGAAGACCCTAATTCAACATTATCTGGTATAGTTTACGTTGACCGAATCGAATTCATC 1980
Db    1915 GGTATACAAACGAATACAAATTTATTTATTTTA---------GACCGAATCGAATTCATC 1965
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Qy   1981 CCAGTAGATGAGACATATGAAGCGGAACAAGATTTAGAAGCAGCGAAGAAAGCAGTGAAT 2040
Db   1966 CCAGTAGATGAGACATATGAAGCGGAAACGGATTTAGAAGCGGCAAAGAAAGCAGTGAAT 2025

Qy   2041 GCCTTGTTTACGAATACAAAAGATGGCTTACGACCAGGCGTAACGGATTATGAAGTGAAT 2100
Db   2026 GCCTTGTTTACGAATACAAAAGATGGATTACAGCCAGGTGTAACGGATTATGAAGTAAAT 2085

Qy   2101 CAAGCGGCAAACTTAGTGGAATGCCTATCGGATGATTTGTATCCAAATGAAAAACGATTG 2160
Db   2086 CAAGCGGCCAACTTAGTGGAATGCCTATCGGATGATTTGTATCCAAATGAAAAACGATTG 2145

Qy   2161 TTATTTGATGCAGTGAGAGAGGCAAAACGCCTCAGTGAGGCACGTAATTTGCTTCAAGAT 2220
Db   2146 TTATTTGATGCAGTGAGAGAGGCAAAACGACTTAGCGAGGCACGGAACTTACTACAAGAT 2205

Qy   2221 CCAGATTTCCAAGAGATAAATGGAGAAAATGGCTGGACGGCAAGTACGGGAATTGAGGTT 2280
Db   2206 CCAGATTTCCAAGAGATAAATGGAGAAAATGGATGGACGGCAAGTACGGGAATTGAGGTT 2265

Qy   2281 ATAGAAGGGGATGCTTTATTCAAAGGGCGTTATCTACGCCTACCAGGTGCGAGAGAAATA 2340
Db   2266 ATAGAAGGGGATGCTGTATTCAAAGGGCGTTATCTACGCCTACCAGGTGCGAGAGAAATA 2325

Qy   2341 GATACGGAAACGTATCCAACGTATCTGTATCAAAAAGTAGAGGAAGGTGTATTAAAACCA 2400
Db   2326 GATACGGAAACGTATCCAACGTATCTGTATCAAAAAGTAGAGGAAGGTGTATTAAAACCA 2385

Qy   2401 TACACAAGATATAGATTGAGAGGGTTTGTCGGAAGCAGTCAAGGATTGGAAATTTTCACA 2460
Db   2386 TACACAAGGTATAGACTGAGAGGATTTGTGGGAAGTAGTCAAGGATTAGAAATTTATACG 2445

Qy   2461 ATTCGTCATCAAACGAACCGAATTGTAAAAAATGTACCGGATGATTTGCTGCCAGATGTA 2520
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Qy   2521 TCTCCTGTTAACTCGGATGGTAGTATCAATCGATGCAGCGAACAAAAGTATGTGAATAGC 2580
Db   2506 CCTCCTGTAAACAATGATGGTAGAATCAATCGATGCAGCGAACAAAAGTATGTGAATAGT 2565

Qy   2581 CGTTTAGAAGTAGAAAACCGTTCTGGTGAAGCGCATGAGTTCTCTATTCCTATTGATACA 2640
Db   2566 CGTTTAGAAGTAGAAAACCGTTCTGGTGAAGCGCATGAGTTCTCAATCCCTATCGATACA 2625

Qy   2641 GGTGAAATCGATTACAATGAAAATGCAGGAATATGGGTTGGATTTAAGATTACGGACCCA 2700
Db   2626 GGAGAGCTGGATTACAATGAAAATGCAGGAATATGGGTTGGATTTAAGATTACGGACCCA 2685

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Db   2686 GAGGGATACGCAACACTTGGAAATCTTGAATTGGTCGAAGAGGGACCTTTGTCAGGAGAC 2745

Qy   2761 GCATTAGAACGCTTGCAAAGAGAAGAACAACAGTGGAAGATTCAAATGACAAGAAGACGT 2820
Db   2746 GCATTAGAACGCTTGCAAAAAGAAGAACAACAGTGGAAGATTCAAATGACAAGAAGACGT 2805

Qy   2821 GAAGAAACAGATAGAAGGTATATGGCATCGAAACAAGCGGTAGATCGTTTATATGCCGAT 2880
Db   2806 GAAGAGACAGATAGAAGATACATGGCATCGAAACAAGCGGTAGATCGTTTATATGCCGAT 2865

Qy   2881 TATCAGGATCAGCAACTGAATCCTGATGTAGAGATTACAGATCTTACTGCGGCCCAAGAT 2940
Db   2866 TATCAGGATCAGCAACTGAATCCGAATGTAGAGATTACAGATCTTACTGCGGCTCAAGAT 2925

Qy   2941 CTGATACAGTCCATTCCTTACGTATATAACGAAATGTTCCCAGAAATACCAGGGATGAAC 3000
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Qy   3001 TATACGAAGTTTACAGAATTAACAGATCGACTCCAACAAGCGTGGAGTTTGTATGATCAG 3060
Db   2986 TATACGAAGTTTACAGAGTTAACAGATCGACTCCAACAAGCCTGGGGATTGTATGATCAA 3045

Qy   3061 CGAAATGCCATACCAAATGGTGATTTTCGAAATGGGTTAAGTAATTGGAATGCAACGCCT 3120

Db   3046 CGAAACGCTATACCAAATGGAGATTACCGAAATGAATTAAGTAATTGGAATACAACATCT 3105

Qy   3121 GGCGTAGAAGTACAACAAATCAATCATACATCTGTCCTTGTGATTCCAAACTGGGATGAG 3180
Db   3106 GGTGTGAATGTACAACAAATCAATCATACATCTGTCCTTGTGATTCCAAACTGGAATGAA 3165

Qy   3181 CAAGTTTCGCAACAGTTTACAGTTCAACCGAATCAAAGATATGTGTTACGAGTTACTGCG 3240
Db   3166 CAAGTTTCACAAAAGTTTACAGTTCAACCGAATCAAAGATATGTGTTACGAGTTACTGCA 3225

Qy   3241 AGAAAAGAAGGGGTAGGAAATGGATATGTAAGTATCCGTGATGGTGGAAATCAAACAGAA 3300
Db   3226 AGAAAAGAAGGGGTAGGAAATGGATATGTAAGTATTCGTGATGGTGGAAATCAATCAGAA 3285

Qy   3301 ACGCTTACTTTTAGTGCAAGCGATTATGATACAAATGGAATGTATAATACGCAAGTGTCC 3360
Db   3286 ACGCTTACTTTTAGTGCAAGCGATTATGATACAAATGGTATGTATGATACACAAGCGTCG 3345

Qy   3361 AATACAAATGGATATAACACAAATAATGCGTATAATACACAAGCATCGAGTACA 3414
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RESULT 2
US-07-876-280-29
; Sequence 29, Application US/07876280
; Patent No. 5262158
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Bagley, Angela L.
; TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates for
; TITLE OF INVENTION: Controlling Acarides
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/876,280
; FILING DATE: 19920430
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3471 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: PS50C
; IMMEDIATE SOURCE:
; CLONE: E. coli NM522(pMYC2320) NRRL B-18769